Amendments to the Specification

Please replace the first full paragraph on page 56 with the following, amended paragraph:

In preferred embodiments, high-precision, contact-printing robots are used to pick up small volumes of dissolved capture agents from the wells of a microtiter plate and to repetitively deliver approximately 1 nL of the solutions to defined locations on the surfaces of substrates, such as chemically-derivatized glass microscope slides. Examples of such robots include the GMS 417 Arrayer, commercially available from Affymetrix of Santa Clara, Calif., and a split pin arrayer constructed according to instructions downloadable from the Brown lab website at ~~http://cmgm.stanford.edu/pbrown~~ cmgm.stanford.edu/pbrown. This results in the formation of microscopic spots of compounds on the slides. It will be appreciated by one of ordinary skill in the art, however, that the current invention is not limited to the delivery of 1 nL volumes of solution, to the use of particular robotic devices, or to the use of chemically derivatized glass slides, and that alternative means of delivery can be used that are capable of delivering picoliter or smaller volumes. Hence, in addition to a high precision array robot, other means for delivering the compounds can be used, including, but not limited to, ink jet printers, piezoelectric printers, and small volume pipetting robots.

Please replace the first full paragraph on page 100 with the following, amended paragraph:

The subject computer generated PETs can also be analyzed according to the likely presence or absence of post-translational modifications. More than 100 different such modifications of amino acid residues are known, examples include but are not limited to acetylation, amidation, deamidation, prenylation (such as farnesylation or geranylation), formylation, glycosylation, hydroxylation, methylation, myristoylation, phosphorylation, ubiquitination, ribosylation and sulphation. Sequence analysis softwares which are capable of determining putative post-translational modification in a given amino acid sequence include the NetPhos server which produces neural network predictions for serine, threonine and tyrosine

phosphorylation sites in eukaryotic proteins (available through ~~http://www.cbs.dtu.dk/services/Net-Phos/~~ the web site at cbs.dtu.dk/services/Net-Phos/), GPI Modification Site Prediction (available through ~~http://mendel.imp.univie.- ac.at/gpi~~ the web site at mendel.imp.univie.- ac.at/gpi) and the ExPASy proteomics server for total protein analysis (available through ~~www.expasy.ch/tools/~~ the web site at expasy.ch/tools/).

Please replace the paragraph bridging pages 112-113 with the following, amended paragraph:

Arginine methylation, a protein modification discovered almost 30 years ago, has recently experienced a renewed interest as several new arginine methyltransferases have been identified and numerous proteins were found to be regulated by methylation on arginine residues. Mowen and David published detailed protocols on Science's STKE (~~www.stke.org/cgi/content/full/OC_sigtrans;2001/93/p11~~ web site at stke.org/cgi/content/full/OC_sigtrans;2001/93/p11) that provide guidelines for the straightforward identification of arginine-methylated proteins, made possible by the availability of novel, commercially available reagents. Specifically, two anti-methylated arginine antibodies are described: mouse monoclonal antibody to methylarginine, clone 7E6 (IgG1) (Abcam, Cambridge, UK) (Data sheet: ~~www.abcam.com/public/ab_detail- .cfm?intAbID=412~~ web site at abcam.com/public/ab_detail- .cfm?intAbID=412, which reacts with mono- and asymmetric dimethylated arginine residues; and mouse monoclonal antibody to methylarginine, clone 21C7 (IgM) (Abcam) (Data sheet: ~~www.abcam.com/public/ab_detail.cfm?intAbI- D=413~~ web site at abcam.com/public/ab_detail.cfm?intAbI- D=413), which reacts with asymmetric dimethylated arginine residues. Detailed protocols for in vitro and in vivo analysis of arginine methylation are provided. See Mowen et al., Cell 104: 731-741, 2001.

Please replace the first full paragraph on page 116 with the following, amended paragraph:

As any one of the total 20 amino acids could be at one specific position of a peptide, the total possible combination for a tetramer (a peptide containing 4 amino acid residues) is 20^4; the total possible combination for a pentamer (a peptide containing 5 amino acid residues) is 20^5 and the total possible combination for a hexamer (a peptide containing 6 amino acid residues) is 20^6. In order to identify unique recognition sequences within the human proteome, each possible tetramer, pentamer or hexamer was searched against the human proteome (total number: 29,076; Source of human proteome: EBI Ensembl project release v 4.28.1 on Mar. 12, 2002, ~~http://www.ensembl.org/Homo_sapiens/~~ web site at ensembl.org/Homo_sapiens/).

Please replace the paragraph bridging pages 117-118 with the following, amended paragraph:

In order to identify pentamer PETs that can be used to, for example, distinguish a specific bacterium from a pool of all other bacteria, each possible pentamer was searched against the NCBI database (~~http://www.ncbi.nlm.nih.gov/PMGifs/Genomes/eub_g.html~~ web site at ncbi.nlm.nih.gov/PMGifs/Genomes/eub_g.html, updated as of Apr. 10, 2002). The results from this analysis are set forth below.

Please replace the second full paragraph on page 121 with the following, amended paragraph:

As indicated above, each possible tetramer, pentamer or hexamer was searched against the human proteome (total number: 29,076; Source of human proteome: EBI Ensembl project release 4.28.1 on Mar. 12, 2002, ~~http://www.ensembl.org/Homo_sapiens/~~ web site at ensembl.org/Homo_sapiens/) to identify unique recognition sequences (PETs).

Please replace the legend on page 123 with the following, amended legend:

*The Sequence IDs used are the ones provided in ~~http://www.ensembl.org/Homo sapiens/~~ the web site at ensembl.org/Homo sapiens/.

Please replace the third full paragraph on page 126 with the following, amended paragraph:

The same approach may be used for other protein families, including GPCRs, proteases, phosphotases, receptors, or specific enzymes. The Human Plasma Membrane Receptome is disclosed at ~~http://receptome.stanford.edu/H- PMR~~ the web site receptome.stanford.edu/H- PMR.

Please replace the first full paragraph on page 127 with the following, amended paragraph:

A total of 2028 Coronavirus peptide sequences were obtained from the NCBI database (~~http://www.ncbi.nlm.nih.gov:80/genomes/SARS/SARS.html~~ web site at ncbi.nlm.nih.gov:80/genomes/SARS/SARS.html). These sequences represent at least 10 different species of Coronavirus. Among them, 1098 non-redundant peptide sequences were identified. Each sequence that appeared identically within (was subsumed in) a larger sequence was removed, leaving the larger sequence as the representative. The resulting sequences were then broken up into overlapping regions of eight amino acids (8-mers), with a sequence difference of 1 amino acid between successive 8-mers. These 8-mers were then queried against a database consisting of all 8-mers similarly generated and present in the proteome of the species in question (or any other set of protein sequences deemed necessary). 8-mers found to be present only once (the sequence identified only itself) were considered unique. The remainder of the sequences were initially classified as non-unique with the understanding that with more in-depth analysis, they might actually be as useful as those sequences initially determined to be unique. For example, an 8-mer may be present in another isoform of its parent sequence, so it would still be

useful in uniquely detecting that parental sequence and that isoform from all other unrelated proteins.